

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently amended). A method for detecting a *Mycobacterium avium* subsp. *paratuberculosis* (Map) infection in an animal, the method comprising the steps of:

(A) providing a biological sample from the animal and extracting nucleic acids from the sample; and

(B) subjecting the biological sample extracted nucleic acids to polymerase chain reaction (PCR) using primers J1 SEQ ID NO: 1 and J2 SEQ ID NO: 2, wherein the presence of an amplification product specific for *Mycobacterium avium* subsp. *paratuberculosis* Map in the polymerase chain reaction PCR reaction mixture indicates that the animal is infected with *Mycobacterium avium* subsp. *paratuberculosis* Map.

2. (Currently amended). The method of claim 1, wherein the *Mycobacterium avium* subsp. *paratuberculosis* Map infection is a subclinical infection.

3. (Original). The method of claim 1, wherein the animal is a cow.

4. (Original). The method of claim 1, wherein the biological sample is blood.

5. (Original). The method of claim 1, wherein the biological sample is milk.

6. (Currently amended). A method for detecting a *Mycobacterium avium* subsp. *paratuberculosis* Map infection in an animal, the method comprising the steps of:

(A) providing a biological sample from the animal and extracting nucleic acids from the sample; and

(B) subjecting the biological sample extracted nucleic acids to nested polymerase chain reaction PCR using at least a first pair of primers for amplifying the IS900 ISO900 region of the *Mycobacterium avium* subsp. *paratuberculosis* Map genome and a second pair of primers for amplifying a portion of the amplified IS900 ISO900 region,

wherein the presence of an amplification product specific for *Mycobacterium avium* subsp. *paratuberculosis* Map in the polymerase chain reaction PCR reaction mixture indicates that the animal is infected with *Mycobacterium avium* subsp. *paratuberculosis* Map.

7. (Original). The method of claim 6, wherein the first pair of primers are primers P90 and P91.

8. (Original). The method of claim 6, wherein the second pair of primers are primers J1 and J2.

9. (Original). The method of claim 7, wherein the second pair of primers are primers J1 and J2.

10. (Original). The method of claim 6, wherein the *Mycobacterium avium* subsp. *paratuberculosis* Map infection is a subclinical infection.

11. (Original). The method of claim 6, wherein the animal is a cow.

12. (Original). The method of claim 6, wherein the biological sample is blood.

13. (Original). The method of claim 6, wherein the biological sample is milk.

14. (Currently amended). The method of claim 6, wherein the at least first set pair of primers consist of the primers P90 and P91, wherein said primers recognize a 413 bp sequence of the IS900 region of the *Mycobacterium avium* subsp. *paratuberculosis*.

15. (Withdrawn). A purified nucleic acid comprising the nucleotide sequence of SEQ ID NO:1.

16. (Withdrawn). A purified nucleic acid comprising the nucleotide sequence of SEQ ID NO:2.

17. (Withdrawn). A kit for detecting a Map infection in an animal, the kit comprising a first pair of primers for amplifying the ISO900 region of the Map genome and a second pair of primers for amplifying a portion of the amplified ISO900 region.

18. (Withdrawn). The kit of claim 17, wherein the first pair of primers are primers P90 and P91.

19. (Withdrawn). The kit of claim 17, wherein the second pair of primers are primers J1 and J2.

20. (Withdrawn). The kit of claim 18, wherein the second pair of primers are primers J1 and J2.